<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/617,334A_

Source: _1FW/6_

Date Processed by STIC: _11/16/06_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 11/16/2006
PATENT APPLICATION: US/10/617,334A   TIME: 09:19:19

Input Set : A:\Xenon 91.txt
Output Set: N:\CRF4\11162006\J617334A.raw

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 5 <110> APPLICANT: Hayden, Michael R.
 6         Brooks-Wilson, Angela R.
 8 <120> TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
10 <130> FILE REFERENCE: 760050-91
12 <140> CURRENT APPLICATION NUMBER: 10/617,334A
13 <141> CURRENT FILING DATE: 2003-07-10
15 <150> PRIOR APPLICATION NUMBER: 09/526,193
16 <151> PRIOR FILING DATE: 2000-03-15
18 <150> PRIOR APPLICATION NUMBER: 60/124,702
19 <151> PRIOR FILING DATE: 1999-03-15
21 <150> PRIOR APPLICATION NUMBER: 60/138,048
22 <151> PRIOR FILING DATE: 1999-06-08
24 <150> PRIOR APPLICATION NUMBER: 60/139,600
25 <151> PRIOR FILING DATE: 1999-06-17
27 <150> PRIOR APPLICATION NUMBER: 60/151,977
28 <151> PRIOR FILING DATE: 1999-09-01
30 <160> NUMBER OF SEQ ID NOS: 290
32 <170> SOFTWARE: PatentIn 3.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2261
36 <212> TYPE: PRT
37 <213> ORGANISM: Homo sapiens
39 <400> SEQUENCE: 1
40 Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
41  1               5                  10                  15
42 Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
43          20                  25                  30
44 Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
45          35                  40                  45
46 Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
47      50                  55                  60
48 Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
49 65                  70                  75                  80
50 Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
51                  85                  90                  95
52 Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
53                 100                 105                 110
54 Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
55              115                 120                 125
56 Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Asn Leu Lys Leu
57          130                 135                 140
58 Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly Phe Leu Tyr His
59 145                 150                 155                 160
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60 Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met Leu Arg Ala Asp
61              165              170              175
62 Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln Leu His Leu Thr
63       .      180       .     185              190
64 Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile Gln Leu Gly Asp
65          195           .     200 '          . 205 .
66 Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Arg Glu Lys Leu Ala Ala
67      210              215              220
68 Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu Lys Pro Ile Leu
69 225              230              235              240
70 Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys Glu Leu Ala Glu
71              245              250              255
72 Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu Ala Gln Glu Leu
73          260              265              270
74 Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu Val Met Phe Leu
75          275              280              285
76 Thr Asn Val Asn Ser Ser Ser Ser Ser Thr Gln Ile Tyr Gln Ala Val
77      290              295              300
78 Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly Leu Lys Ile Lys
79 305              310              315              320
80 Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala Leu Phe Gly Gly
81              325              330              335
82 Asn Gly Thr Glu Glu Asp Ala Glu Thr Phe Tyr Asp Asn Ser Thr Thr
83          340              345              350
84 Pro Tyr Cys Asn Asp Leu Met Lys Asn Leu Glu Ser Ser Pro Leu Ser
85          355              360              365
86 Arg Ile Ile Trp Lys Ala Leu Lys Pro Leu Leu Val Gly Lys Ile Leu
87      370              375              380
88 Tyr Thr Pro Asp Thr Pro Ala Thr Arg Gln Val Met Ala Glu Val Asn
89 385              390              395              400
90 Lys Thr Phe Gln Glu Leu Ala Val Phe His Asp Leu Glu Gly Met Trp
91              405              410              415
92 Glu Glu Leu Ser Pro Lys Ile Trp Thr Phe Met Glu Asn Ser Gln Glu
93          420 '            425              430
94 Met Asp Leu Val Arg Met Leu Leu Asp Ser Arg Asp Asn Asp His Phe
95          435              440              445
96 Trp Glu Gln Gln Leu Asp Gly Leu Asp Trp Thr Ala Gln Asp Ile Val
97      450              455              460
98 Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser Ser Asn Gly Ser
99 465              470              475              480
100 Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu. Thr Asn Gln Ala Ile Arg
101              485              490              495
102 Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn Lys Leu Glu Pro
103          500              505              510
104 Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met Glu Leu Leu Asp
105          515              520              525
106 Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly Ile Thr Pro Gly
107      530              535              540
108 Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile Arg Met Asp Ile
```

```
109 545                   550                   555                   560
110 Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly Tyr Trp Asp Pro
111                   565                   570                   575 .
112 Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Arg Tyr Val Trp Gly Gly
113                   580                   585                   590
114 Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile Ile Arg Val Leu
115             595                   600                   605
116 Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln Gln Met Pro Tyr
117       610                   615                   620
118 Pro Cys Tyr Val Asp Asp Ile Phe Leu Arg Val Met Ser Arg Ser Met
119 625                   630                   635                   640
120 Pro Leu Phe Met Thr Leu Ala Trp Ile Tyr Ser Val Ala Val Ile Ile
121                   645                   650                   655
122 Lys Gly Ile Val Tyr Glu Lys Glu Ala Arg Leu Lys Glu Thr Met Arg
123             660                   665                   670
124 Ile Met Gly Leu Asp Asn Ser Ile Leu Trp Phe Ser Trp Phe Ile Ser
125             675                   680                   685         .
126 Ser Leu Ile Pro Leu Leu Val Ser Ala Gly Leu Leu Val Val Ile Leu
127       690                   695                   700
128 Lys Leu Gly Asn Leu Leu Pro Tyr Ser Asp Pro Ser Val Val Phe Val
129 705                   710                   715             .     720
130 Phe Leu Ser Val Phe Ala Val Val Thr Ile Leu Gln Cys Phe Leu Ile
131                   725                   730                   735
132 Ser Thr Leu Phe Ser Arg Ala Asn Leu Ala Ala Ala Cys Gly Gly Ile
133       .           740                   745                   750
134 Ile Tyr Phe Thr Leu Tyr Leu Pro Tyr Val Leu Cys Val Ala Trp Gln
135             755                   760         .           765
136 Asp Tyr Val Gly Phe Thr Leu Lys Ile Phe Ala Ser Leu Leu Ser Pro
137       770                   775                   780
138 Val Ala Phe Gly Phe Gly Cys Glu Tyr Phe Ala Leu Phe Glu Glu Gln
139 785                   790                   795             · 800
140 Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser Pro Val Glu Glu
141                   805                   810                   815
142 Asp Gly Phe Asn Leu Thr Thr Ser Val Ser Met Met Leu Phe Asp Thr
143             820                   825 ·                 830
144 Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala Val Phe Pro Gly
145             835                   840                   845
146 Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys Thr Lys Ser Tyr
147       850                   855                   860
148 Trp Phe Gly Glu Glu Ser Asp Glu Lys Ser His Pro Gly Ser Asn Gln
149 865                   870                   875                   880
150 Lys Arg Ile Ser Glu Ile Cys Met Glu Glu Glu Pro Thr His Leu Lys
151                   885                   890                   895
152 Leu Gly Val Ser Ile Gln Asn Leu Val Lys Val Tyr Arg Asp Gly Met
153             900                   905                   910
154 Lys Val Ala Val Asp Gly Leu Ala Leu Asn Phe Tyr Glu Gly Gln Ile
155             915                   920                   925
156 Thr Ser Phe Leu Gly His Asn Gly Ala Gly Lys Thr Thr Thr Met Ser
157       930                   935                   940
```

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158 Ile Leu Thr Gly Leu Phe Pro Pro Thr Ser Gly Thr Ala Tyr Ile Leu
159 945                     950                 955                 960
160 Gly Lys Asp Ile Arg Ser Glu Met Ser Thr Ile Arg Gln Asn Leu Gly
161                     965                 970                 975
162 Val Cys Pro Gln His Asn Val Leu Phe Asp Met Leu Thr Val Glu Glu
163                     980                 985                 990
164 His Ile Trp Phe Tyr Ala Arg Leu Lys Gly Leu Ser Glu Lys His Val
165             995                 1000                1005
166 Lys Ala Glu Met Glu Gln Met Ala Leu Asp Val Gly Leu Pro Ser Ser
167       1010                1015                1020
168 Lys Leu Lys Ser Lys Thr Ser Gln Leu Ser Gly Gly Met Gln Arg Lys
169 1025                1030                1035                1040
170 Leu Ser Val Ala Leu Ala Phe Val Gly Gly Ser Lys Val Val Ile Leu
171                 1045                1050                1055
172 Asp Glu Pro Thr Ala Gly Val Asp Pro Tyr Ser Arg Arg Gly Ile Trp
173             1060                1065                1070
174 Glu Leu Leu Leu Lys Tyr Arg Gln Gly Arg Thr Ile Ile Leu Ser Thr
175       1075                1080                1085
176 His His Met Asp Glu Ala Asp Val Leu Gly Asp Arg Ile Ala Ile Ile
177       1090                1095                1100
178 Ser His Gly Lys Leu Cys Cys Val Gly Ser Ser Leu Phe Leu Lys Asn
179 1105                1110                1115                1120
180 Gln Leu Gly Thr Gly Tyr Tyr Leu Thr Leu Val Lys Lys Asp Val Glu
181                 1125                1130                1135
182 Ser Ser Leu Ser Ser Cys Arg Asn Ser Ser Ser Thr Val Ser Tyr Leu
183                 1140                1145                1150
184 Lys Lys Glu Asp Ser Val Ser Gln Ser Ser Ser Asp Ala Gly Leu Gly
185       1155                1160                1165
186 Ser Asp His Glu Ser Asp Thr Leu Thr Ile Asp Val Ser Ala Ile Ser
187       1170                1175                1180
188 Asn Leu Ile Arg Lys His Val Ser Glu Ala Arg Leu Val Glu Asp Ile
189 1185                1190                1195                1200
190 Gly His Glu Leu Thr Tyr Val Leu Pro Tyr Glu Ala Ala Lys Glu Gly
191                 1205                1210                1215
192 Ala Phe Val Glu Leu Phe His Glu Ile Asp Asp Arg Leu Ser Asp Leu
193             1220                1225                1230
194 Gly Ile Ser Ser Tyr Gly Ile Ser Glu Thr Thr Leu Glu Glu Ile Phe
195       1235                1240                1245
196 Leu Lys Val Ala Glu Glu Ser Gly Val Asp Ala Glu Thr Ser Asp Gly
197       1250                1255                1260
198 Thr Leu Pro Ala Arg Arg Asn Arg Arg Ala Phe Gly Asp Lys Gln Ser
199 1265                1270                1275                1280
200 Cys Leu Arg Pro Phe Thr Glu Asp Asp Ala Ala Asp Pro Asn Asp Ser
201                 1285                1290                1295
202 Asp Ile Asp Pro Glu Ser Arg Glu Thr Asp Leu Leu Ser Gly Met Asp
203             1300                1305                1310
204 Gly Lys Gly Ser Tyr Gln Val Lys Gly Trp Lys Leu Thr Gln Gln Gln
205       1315                1320                1325
206 Phe Val Ala Leu Leu Trp Lys Arg Leu Leu Ile Ala Arg Arg Ser Arg
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207      1330             1335             1340
208 Lys Gly Phe Phe Ala Gln Ile Val Leu Pro Ala Val Phe Val Cys Ile
209 1345             1350             1355             1360
210 Ala Leu Val Phe Ser Leu Ile Val Pro Pro Phe Gly Lys Tyr Pro Ser
211              1365             1370             1375
212 Leu Glu Leu Gln Pro Trp Met Tyr Asn Glu Gln Tyr Thr Phe Val Ser
213              1380             1385             1390
214 Asn Asp Ala Pro Glu Asp Thr Gly Thr Leu Glu Leu Leu Asn Ala Leu
215         1395             1400             1405
216 Thr Lys Asp Pro Gly Phe Gly Thr Arg Cys Met Glu Gly Asn Pro Ile
217      1410             1415             1420
218 Pro Asp Thr Pro Cys Gln Ala Gly Glu Glu Glu Trp Thr Thr Ala Pro
219 1425             1430             1435             1440
220 Val Pro Gln Thr Ile Met Asp Leu Phe Gln Asn Gly Asn Trp Thr Met
221              1445             1450             1455
222 Gln Asn Pro Ser Pro Ala Cys Gln Cys Ser Ser Asp Lys Ile Lys Lys
223         1460             1465             1470
224 Met Leu Pro Val Cys Pro Pro Gly Ala Gly Gly Leu Pro Pro Pro Gln
225         1475             1480             1485
226 Arg Lys Gln Asn Thr Ala Asp Ile Leu Gln Asp Leu Thr Gly Arg Asn
227      1490             1495             1500
228 Ile Ser Asp Tyr Leu Val Lys Thr Tyr Val Gln Ile Ile Ala Lys Ser
229 1505             1510             1515             1520
230 Leu Lys Asn Lys Ile Trp Val Asn Glu Phe Arg Tyr Gly Gly Phe Ser
231              1525             1530             1535
232 Leu Gly Val Ser Asn Thr Gln Ala Leu Pro Pro Ser Gln Glu Val Asn
233         1540             1545             1550
234 Asp Ala Ile Lys Gln Met Lys Lys His Leu Lys Leu Ala Lys Asp Ser
235         1555             1560             1565
236 Ser Ala Asp Arg Phe Leu Asn Ser Leu Gly Arg Phe Met Thr Gly Leu
237      1570             1575             1580
238 Asp Thr Arg Asn Asn Val Lys Val Trp Phe Asn Asn Lys Gly Trp His
239 1585             1590             1595             1600
240 Ala Ile Ser Ser Phe Leu Asn Val Ile Asn Asn Ala Ile Leu Arg Ala
241              1605             1610             1615
242 Asn Leu Gln Lys Gly Glu Asn Pro Ser His Tyr Gly Ile Thr Ala Phe
243         1620             1625             1630
244 Asn His Pro Leu Asn Leu Thr Lys Gln Gln Leu Ser Glu Val Ala Leu
245         1635             1640             1645
246 Met Thr Thr Ser Val Asp Val Leu Val Ser Ile Cys Val Ile Phe Ala
247      1650             1655             1660
248 Met Ser Phe Val Pro Ala Ser Phe Val Val Phe Leu Ile Gln Glu Arg
249 1665             1670             1675             1680
250 Val Ser Lys Ala Lys His Leu Gln Phe Ile Ser Gly Val Lys Pro Val
251              1685             1690             1695
252 Ile Tyr Trp Leu Ser Asn Phe Val Trp Asp Met Cys Asn Tyr Val Val
253              1700             1705             1710
254 Pro Ala Thr Leu Val Ile Ile Ile Phe Ile Cys Phe Gln Gln Lys Ser
255      1715             1720             1725
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/16/2006
PATENT APPLICATION: US/10/617,334A   TIME: 09:19:20

Input Set : **A:\Xenon 91.txt**
Output Set: **N:\CRF4\11162006\J617334A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; N Pos. 9965,9966,9967,9968,9969,9970
Seq#:19; N Pos. 251
Seq#:21; N Pos. 19998
Seq#:29; N Pos. 1,5,6,10,15,24,25,26,27,28,34,37,38,42,43,46,48,49,50,67,72
Seq#:29; N Pos. 80,84,91,97,99,102,113,117,122,125,135
Seq#:39; N Pos. 8
Seq#:54; N Pos. 14,15,18,20,22,23,25
Seq#:61; N Pos. 13,15,16,18,20,21
Seq#:69; N Pos. 8

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/617,334A**

DATE: 11/16/2006
TIME: 09:19:20

Input Set : **A:\Xenon 91.txt**
Output Set: **N:\CRF4\11162006\J617334A.raw**

```
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:9960
L:1000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:240
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:19980
L:2069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:2241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:2367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:2428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:2497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
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